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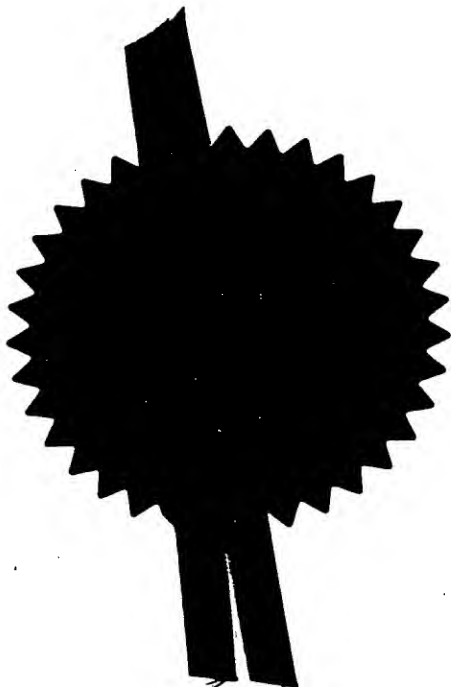
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Your Reference: B45110

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① Title of invention

1 Please give the title of the invention VACCINE

② Applicant's details
☐ First or only applicant

2a If you are applying as a corporate body please give:
Corporate Name SmithKline Beecham Biologicals s.a.

Country (and State of incorporation, if appropriate) Belgium

2b If you are applying as an individual or one of a partnership please give in full:

Surname
Forenames

2c In all cases, please give the following details:

Address: Rue de l'institut 89, B-1330, Rixensart

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(if applicable)

Country Belgium
ADP number 5800974002
(if known)

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④ Reference number

4. Agent's or
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⑤ Claiming an earlier application date

5. Are you claiming that this application be treated as having been filed on the date of filing of an earlier application?

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7

- any applicant is not an inventor
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- any applicant is a corporate body.

8 Please supply duplicates of claim(s), abstract, description and drawings).

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9 You or your appointed agent (see Rule 90 of the Patents Rules 1990) must sign this request.

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A completed fee sheet should preferably accompany the fee.

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Yes ☐

No ☒

A Statement of Inventorship on Patents form 7/77 will need to be filed (see Rule 15).).

8 Checklist

8a Please fill in the number of sheets for each of the following types of document contained in this application

Continuation sheets for this Patents Form 1/77

Claim(s)

2

Description

19

Abstract

Drawing(s)

7

8b Which of the following documents also accompanies the application?

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Patents Form 7/77 - Statement of Inventorship and Right to Grant

Patents Form 9/77 - Preliminary Examination Report

Patents Form 10/77 - Request for Substantive Examination

9 Request

I/We request the grant of a patent on the basis of this application.

Signed

Marcus J W Dalton

Date:

26/09/97

(day

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MARCUS J W DALTON
Chartered Patent Attorney
Attorney for the Applicant

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VACCINE

5 The present invention relates to novel HIV protein constructs, to their use in medicine, to pharmaceutical compositions containing them and to methods of their manufacture.

In particular, the invention relates to fusion proteins comprising HIV-1 NEF and/or TAT proteins.

10 HIV-1 is the primary cause of the acquired immune deficiency syndrome (AIDS) which is regarded as one of the world's major health problems. Although extensive research throughout the world, has been conducted to produce a vaccine, such efforts thus far, have not been successful.

Non-envelope proteins of HIV-1 have been described and include for example internal structural proteins such as the products of the *gag* and *pol* genes and, other non-structural proteins such as Rev, Nef, Vif and Tat (Greene et al., 15 New England J. Med, 324, 5, 308 et seq (1991) and Bryant et al. (Ed. Pizzo), Pediatr. Infect. Dis. J., 11, 5, 390 et seq (1992).

HIV NEF and TAT proteins are early proteins, that is they are expressed early in infection and in the absence of structural proteins.

20 According to the present invention there is provided a NEF or TAT protein derived from *Pichia Pastoris*. In one embodiment the NEF or TAT proteins are linked to an immunological fusion protein.

Preferably the fusion protein is protein D or it lipidated derivative Lipoprotein D, from *Haemophilus influenzae* B. In particular, it is preferred that 25 the N-terminal third, i.e. approximately the first 100-130 amino acids are utilised. Alternatively and in a preferred embodiment the NEF protein may be linked to the TAT proteins. Such NEF-TAT fusions may optionally also be linked to an immunological fusion partner, such as protein D.

The proteins of the present invention preferably contain a C terminal 30 Histidine tail which comprises between 5-10 Histidine residues. This aids purification. In an embodiment of the invention, NEF-TAT fusion proteins are optionally linked to a non HIV immunological fusion partner. Preferred constructs

Enzymatic polymerisation of DNA may be carried out *in vitro* using a DNA polymerase such as DNA polymerase I (Klenow fragment) in an appropriate buffer containing the nucleoside triphosphates dATP, dCTP, dGTP and dTTP as required at a temperature of 10°-37°C, generally in a volume of 50µl or less. Enzymatic

5 ligation of DNA fragments may be carried out using a DNA ligase such as T4 DNA ligase in an appropriate buffer, such as 0.05M Tris (pH 7.4), 0.01M MgCl₂, 0.01M dithiothreitol, 1mM spermidine, 1mM ATP and 0.1mg/ml bovine serum albumin, at a temperature of 4°C to ambient, generally in a volume of 50ml or less. The chemical synthesis of the DNA polymer or fragments may be carried out by

10 conventional phosphotriester, phosphite or phosphoramidite chemistry, using solid phase techniques such as those described in 'Chemical and Enzymatic Synthesis of Gene Fragments - A Laboratory Manual' (ed. H.G. Gassen and A. Lang), Verlag Chemie, Weinheim (1982), or in other scientific publications, for example M.J. Gait, H.W.D. Matthes, M. Singh, B.S. Sproat, and R.C. Titmas, Nucleic Acids

15 Research, 1982, 10, 6243; B.S. Sproat, and W. Bannwarth, Tetrahedron Letters, 1983, 24, 5771; M.D. Matteucci and M.H. Caruthers, Tetrahedron Letters, 1980, 21, 719; M.D. Matteucci and M.H. Caruthers, Journal of the American Chemical Society, 1981, 103, 3185; S.P. Adams *et al.*, Journal of the American Chemical Society, 1983, 105, 661; N.D. Sinha, J. Biernat, J. McMannus, and H. Koester,

20 Nucleic Acids Research, 1984, 12, 4539; and H.W.D. Matthes *et al.*, EMBO Journal, 1984, 3, 801.

The process of the invention may be performed by conventional recombinant techniques such as described in Maniatis *et al.*, Molecular Cloning - A Laboratory Manual; Cold Spring Harbor, 1982-1989.

25 In particular, the process may comprise the steps of :

- i) preparing a replicable or integrating expression vector capable, in a host cell, of expressing a DNA polymer comprising a nucleotide sequence that encodes the protein or
- 30 an immunogenic derivative thereof
- ii) transforming a host cell with said vector

described in, for example, Maniatis *et al.* cited above, or "DNA Cloning" Vol. II, D.M. Glover ed., IRL Press Ltd, 1985.

5 The choice of transforming conditions is determined by the host cell. Thus, a bacterial host such as *E. coli* may be treated with a solution of CaCl_2 (Cohen *et al.*, Proc. Nat. Acad. Sci., 1973, 69, 2110) or with a solution comprising a mixture of RbCl , MnCl_2 , potassium acetate and glycerol, and then with 3-[N-morpholino]-propane-sulphonic acid, RbCl and glycerol. Mammalian cells in culture may be transformed by calcium co-precipitation of the vector DNA onto the cells. The invention also extends to a host cell transformed with a replicable expression vector
10 of the invention.

Culturing the transformed host cell under conditions permitting expression of the DNA polymer is carried out conventionally, as described in, for example, Maniatis *et al.* and "DNA Cloning" cited above. Thus, preferably the cell is supplied with nutrient and cultured at a temperature below 50°C .

15 The product is recovered by conventional methods according to the host cell. Thus, where the host cell is bacterial, such as *E. coli* - or yeast such as *Pichia*; it may be lysed physically, chemically or enzymatically and the protein product isolated from the resulting lysate. Where the host cell is mammalian, the product may generally be isolated from the nutrient medium or from cell free extracts.
20 Conventional protein isolation techniques include selective precipitation, adsorption chromatography, and affinity chromatography including a monoclonal antibody affinity column.

As the proteins of the present invention are provided with Histidine tails, purification can easily be achieved by the use of a metal ion affinity column. In a
25 preferred embodiment, the protein is further purified by subjecting it to cation ion exchange chromatography and/or Gel filtration chromatography. The protein is then sterilised by passing through a $0.22\ \mu\text{m}$ membrane.

The proteins of the invention can then be formulated as a vaccine, or the Histidine residues enzymatically cleared.

Preferably the formulation additional comprises an oil in water emulsion and tocopherol. The present invention also provides a method for producing a vaccine formulation comprising mixing a protein of the present invention together with a pharmaceutically acceptable excipient, such as 3D-MPL.

- 5 The vaccine of the present invention may additional comprise further HIV proteins, such as the envelope glycoprotein gp160 or its derivative gp 120.

The invention will be further described by reference to the following examples:

10 **EXAMPLES:**

General

- 15 Nef and Tat proteins, two regulatory proteins encoded by the human immunodeficiency virus (HIV-1) were produced in *E.coli* and in the methylotrophic yeast *Pichia pastoris*.

The Nef gene from the Bru/Lai isolate (Cell 40: 9-17, 1985) was selected for these constructs since this gene is among those that are most closely related to the consensus Nef .

- 20 The starting material for the Bru/Lai Nef gene was a 1170bp DNA fragment cloned on the mammalian expression vector pcDNA3 (pcDNA3/Nef).

The Tat gene originates from the BH10 molecular clone. This gene was received as an HTLV III cDNA clone named pCV1 and described in Science, 229, p69-73, 1985.

25

1. EXPRESSION OF HIV-1 NEF AND TAT SEQUENCES IN E.COLI.

- Sequences encoding the Nef protein as well as a fusion of Nef and Tat sequences were placed in plasmids vectors: pRIT14586 and pRIT14589
30 (see figure 1).

NcoI

PRIMER 01: 5' ATCGTCCATG.GGT.GGC.AAG.TGG.T 3'

5

SpeI

PRIMER 02: 5' CGGCTACTAGTGCAGTTCTTGAA 3'

The Nef DNA region amplified starts at nucleotide 8357 and terminates at nucleotide 8971 (Cell, 40: 9-17, 1985).

- 10 An NcoI restriction site (with carries the ATG codon of the Nef gene) was introduced at the 5' end of the PCR fragment while a SpeI site was introduced at the 3' end.

- The PCR fragment obtained and the expression plasmid pRIT14586 were both restricted by NcoI and SpeI, purified on an agarose gel, ligated and transformed in 15 the appropriate *E. coli* host cell, strain AR58. This strain is a cryptic λ lysogen derived from N99 that is *galE::Tn10*, Δ -8 (*chlD-pgl*), Δ -H1 (*cro-chlA*), N^+ , and *ci857*.

- The resulting recombinant plasmid received, after verification of the Nef amplified region by automatic sequencing, (see section 1.1.2 below) the pRIT14595 20 denomination.

1.1.2 Selection of transformants of *E. Coli* strain AR58 with pRIT14595

- 25 When transformed in AR58 *E. coli* host strain, the recombinant plasmid directs the heat-inducible production of the heterologous protein.

- Heat inducible protein production of several recombinant lipoD-Nef-His transformants was analysed by Coomassie Blue stained SDS-PAGE. All the transformants analysed showed an heat inducible heterologous protein production. The abundance of the recombinant Lipo D-Nef-Tat-His fusion protein was estimated 30 at 10% of total protein.

1.3 CONSTRUCTION OF RECOMBINANT STRAIN ECLD-NT6 PRODUCING THE LIPOD-NEF-TAT-HIS FUSION PROTEIN.

5 1.3.1 Construction of the lipoD-Nef-Tat-His expression plasmid pRIT14596

The Tat gene(BH10 isolate) was amplified by PCR from a derivative of the pCV1 plasmid with primers 03 and 04. SpeI restriction sites were introduced at both ends of the PCR fragment.

10

SpeI

PRIMER 03: 5' ATCGTACTAGT.GAG.CCA.GTA.GAT.C 3'

SpeI

15 PRIMER 04: 5' CGGCTACTAGTTTTCCTTCGGGCCT 3'

The nucleotide sequence of the amplified Tat gene is illustrated in the pCV1 clone (Science 229 : 69-73, 1985) and covers nucleotide 5414 till nucleotide 7998. The PCR fragment obtained and the plasmid pRIT14595 (expressing lipoD-Nef-His protein) were both digested by SpeI restriction enzyme, purified on an agarose gel, ligated and transformed in competent AR58 cells. The resulting recombinant plasmid received, after verification of the Tat amplified sequence by automatic sequencing (see section 1.3.2 below), the pRIT14596 denomination.

25 1.3.2 Selection of transformants of strain AR58 with pRIT14596

Transformants were grown, heat induced and their proteins were analysed by Coomassie Blue stained gels. The production level of the recombinant protein was estimated at 1 % of total protein. One recombinant strain was selected and received the laboratory denomination ECLD-NT6.

30

To express these HIV-1 genes a modified version of the integrative vector PHIL-D2 (INVITROGEN) was used. This vector was modified in such a way that expression of heterologous protein starts immediately after the native ATG codon of the AOX1 gene and will produce recombinant protein with a tail of one glycine and

5

six histidines residues . This PHIL-D2-MOD vector was constructed by cloning an oligonucleotide linker between the adjacent *AsuII* and *EcoRI* sites of PHIL-D2 vector. In addition to the His tail, this linker carries *NcoI*, *SpeI* and *XbaI* restriction sites between which Nef, Tat and Nef-Tat fusion were inserted.

10

2.1 CONSTRUCTION OF THE INTEGRATIVE VECTORS pRIT14597
(encoding Nef-His protein), pRIT14598 (encoding Tat-His protein) and pRIT14599 (encoding fusion Nef-Tat-His).

The Nef gene was amplified by PCR from the pcDNA3/Nef plasmid with
15 primers 01 and 02(see section 1.1.1 construction of pRIT14595). The PCR fragment obtained and the integrative PHIL-D2-MOD vector were both restricted by *NcoI* and *SpeI*, purified on agarose gel and ligated to create the integrative plasmid pRIT14597.

The Tat gene was amplified by PCR from a derivative of the pCV1 plasmid
20 with primers 05 and 04(see section 1.3.1 construction of pRIT14596):

NcoI

PRIMER 05 5'ATCGTCCATGGAGCCAGTAGATC 3'

25 An *NcoI* restriction site was introduced at the 5' end of the PCR fragment while a *SpeI* site was introduced at the 3' end with primer 04. The PCR fragment obtained and the PHIL-D2-MOD vector were both restricted by *NcoI* and *SpeI*, purified on agarose gel and ligated to create the integrative plasmid pRIT14598.

To construct pRIT14599, a 910bp DNA fragment corresponding to the Nef-
30 Tat-His coding sequence was ligated between the *EcoRI* blunted(T4 polymerase)

- °A threonine and a serine introduced by cloning procedure

- °One glycine and six histidines

5 Strain Y1737(Mut^s phenotype) producing the recombinant Nef-Tat-His fusion protein, a myristylated 302 amino acids protein which is composed of:

- °Myristic acid

- °A methionine, created by the use of NcoI cloning site

10 °205a.a. of Nef protein(starting at a.a.2 and extending to a.a.206)

- °A threonine and a serine created by the cloning procedure

- °85a.a. of the Tat protein(starting at a.a.2 and extending to a.a.86)

- °A threonine and a serine introduced by the cloning procedure

- °One glycine and six histidines

Carboxymethylation
(1/2 h - room temperature - in the dark)



Immobilized metal ion affinity
chromatography on Ni⁺⁺-NTA-Agarose
(Qiagen - 30 ml of resin)

+ 0,25M Iodoacetamid (powder addition) / pH
adjusted to 7.5 (with 0,5M NaOH solution) before
incubation

Equilibration buffer: 10 mM PO₄ pH 7.5 - 150m
NaCl - 4.0M GuHCl

Washing buffer: 1) Equilibration buffer

2) 10 mM PO₄ pH 7.5 - 150mM
NaCl - 6M Urea

3) 10 mM PO₄ pH 7.5 - 150mM
NaCl - 6M Urea - 25 mM
Imidazol

Elution buffer: 10 mM PO₄ pH 7.5 - 150mM Na
- 6M Urea - 0,5M Imidazol



Dilution

Down to an ionic strength of 18 mS/cm²

Dilution buffer: 10 mM PO₄ pH 7.5 - 6M Urea



Cation exchange chromatography on SP
Sephacrose FF
(Pharmacia - 30 ml of resin)

Equilibration buffer: 10 mM PO₄ pH 7.5 -
150mM NaCl - 6.0M Urea

Washing buffer: 1) Equilibration buffer

2) 10 mM PO₄ pH 7.5 - 250m
NaCl - 6M Urea

Elution buffer: 10 mM Borate pH 9.0 - 2M NaCl
6M Urea -



Concentration

up to 5 mg/ml

10kDa Omega membrane(Filtron)



Gel filtration chromatography on
Superdex200 XK 16/60
(Pharmacia - 120 ml of resin)

Elution buffer: 10 mM PO₄ pH 7.5 - 150mM Na
- 6M Urea



Dialysis
(O/N - 4°C)

Buffer: 10 mM PO₄ pH 6.8 - 150mM NaCl -
Arginin*

Experiments performed at Smith Kline Beecham Biologicals have demonstrated a clear synergistic effect of combinations of MPL and QS21 in the induction of both humoral and TH1 type cellular immune responses.

- 5 **The oil/water emulsion** is composed of 2 oils (a tocopherol and squalene), and of PBS containing Tween 80 as emulsifier. The emulsion comprised 5% squalene 5% tocopherol 0.4% Tween 80 and had an average particle size of 180 nm and is known as SB62 (see WO 95/17210).

- Experiments performed at Smith Kline Beecham Biologicals have proven that the
10 adjunction of this O/W emulsion to MPL/QS21 further increases their immunostimulant properties.

Preparation of emulsion SB62 (2 fold concentrate)

- 15 Tween 80 is dissolved in phosphate buffered saline (PBS) to give a 2% solution in the PBS. To provide 100 ml two fold concentrate emulsion 5g of DL alpha tocopherol and 5ml of squalene are vortexed to mix thoroughly. 90ml of PBS/Tween solution is added and mixed thoroughly. The resulting emulsion is then passed through a syringe and finally microfluidised by using an M110S
20 microfluidics machine. The resulting oil droplets have a size of approximately 180 nm.

Preparation of oil in water formulation.

- 25 Antigen prepared in accordance with example 1 or 2 (5 μ g) was diluted in 10 fold concentrated PBS pH 6.8 and H₂O before consecutive addition of SB62, 3 D MPL (5 μ g), QS21 (5 μ g) and 50 μ g/ml thiomersal as preservative at 5 min interval. The emulsion volume is equal to 50% of the total volume (50 μ l for a dose of 100 μ l).
30 All incubations were carried out at room temperature with agitation.

* FIGURE 2

◇ Pichia-expressed constructs (plain constructs)5 ⇒ NEF - HISDNA sequence

ATGGGTGGCAAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGA
 10 ATGAGACGAGCTGAGCCAGCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTGGAA
 AAACATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGG
 CTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTA
 AGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGG
 GGACTGGAAGGGCTAATTCCTCCCAACGAAGACAAGATATCCTTGATCTGTGGATC
 15 TACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGGTC
 AGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAG
 GTAGAAGAGGCCAATAAAGGAGAGAAACACCAGCTTGTTACACCCTGTGAGCCTGCAT
 GGAATGGATGACCCTGAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCA
 TTTTCATCACGTGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGGC
 20 CACCATCACCATCACCATTAA

Protein sequence

MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAW
 25 LEAQEEEEVGFVPTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDWI
 YHTQGYFPDWQNYTPGPGVRYPLTFGWICYKLPVEPDKVEEANKGENTSLLHPVSLH
 GMDDPEREVLEWRFD SRLAFHHVARELHPEYFKNCTSGHHHHHH.

30 ⇒ TAT - HISDNA sequence

ATGGAGCCAGTAGATCCTAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAA
 35 ACTGCTTGTAACCAATTGCTATTGTAAAAAGTGTTGCTTTCATTGCCAAGTTTGTTTC
 ATAACAAAAGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGA
 CCTCCTCAAGGCAGTCAGACTCATCAAGTTTCTCTATCAAAGCAACCCACCTCCCAA
 TCCCGAGGGGACCCGACAGGCCCCGAAGGAACTAGTGGCCACCATCACCATCACCAT
 TAA

40

Protein sequence

MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRR
 PPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH.

45

*

5 ATGGATCCAAAACTTTAGCCCTTTCTTTATTAGCAGCTGGCGTACTAGCAGGTTGT
 AGCAGCCATTTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAAATCATTATT
 GCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATACGTTAGAATCTAAAGCACTT
 10 GCTTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACTAAGGATGGT
 CGTTTAGTGGTTATTCACGATCACTTTTTAGATGGCTTGACTGATGTTGCGAAAAAA
 TTCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTTACCTTAAAA
 GAAATTCAAAGTTTAGAAATGACAGAAAACTTTGAAACCATGGGTGGCAAGTGGTCA
 AAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGAATGAGACGAGCTGAGCCA
 15 GCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTGGAAAAACATGGAGCAATCACA
 AGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGGCTAGAAGCACAAGAGGAG
 GAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATGACTTACAAG
 GCAGCTGTAGATCTTAGCCACTTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATT
 CACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAAGGCTAC
 20 TCCCTGATTGGCAGAACTACACACCAGGGGCCAGGGGTCAGATATCCACTGACCTTT
 GGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAGGCCAATAAA
 GGAGAGAACACCAGCTTGTTACACCTGTGAGCCTGCATGGAATGGATGACCCTGAG
 AGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTTCATCACGTGGCCCGA
 GAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGGCCACCATCACCATCACCAT
 TAA

Protein sequence of the processed lipidated ProtD-NEF-HIS protein

(Amino-acids corresponding to Prot D fusion partner are in bold)

25 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFQAQADYLEQDLAMTKD
 GRLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKW
 SKSSVVGWPTVRERMRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQE
 30 EEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDWYHTQG
 YFPDWQNYTPGPGVRYPLTFGWCYKLPVEPDKVEEANKGENTSLLHPVSLHGMDDP
 EREVLEWRFD SRLAFHHVARELHPEYFKNCTSGHHHHHH.

35 ⇒ LipoD-NEF-TAT-HIS

DNA sequence

Nucleotides corresponding to the Prot D Fusion Partner are in bold.

40 The Lipidation Signal Sequence is underlined. After processing, the cysteine coded by the
 TGT codon, indicated with a star, becomes the amino terminal residue which is then modified
 by covalently bound fatty acids.

ATGGATCCAAGCAGCCATTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAA
 ATCATTATTGCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATAACGTTAGAATCT
 AAAGCACTTGCGTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACT
 5 AAGGATGGTCGTTTAGTGTTATTCACGATCACTTTTATAGATGGCTTGACTGATGTT
 GCGAAAAAATTCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTT
 ACCTTAAAAGAAATTCAAAGTTTAGAAATGACAGAAAACCTTGAAACCATGGGTGGC
 AAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGAATGAGACGA
 GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTGGAAAAACATGGA
 10 GCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGGCTAGAAGCA
 CAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATG
 ACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTTAAAAGAAAAGGGGGGACTGGAA
 GGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACA
 CAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGGTGAGATATCCA
 15 CTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAG
 GCCAATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGAT
 GACCCTGAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTTCATCAC
 GTGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGGCCACCATCAC
 CATCACCATTAA
 20

Protein sequence

(Amino-acids corresponding to Prot D fusion partner are
 25 in bold)

MDPSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFQAQADYLEQDLAMT
 KDGRLLVVIHDHFLDGLTDVAKKFPHRHRKDRYYVIDFTLKEIQSLEMTENFETMGG
 KWSKSSVVGWPTVRERMRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
 30 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLDWIYHT
 QGYFPDWQNYTPGPGVRYPLTFGWICYKLVPEPDKVEEANKGENTSLLHPVSLHGMD
 DPEREVLEWRFD SRLAFHHVARELHPEYFKNCTSGHHHHH.

35 \Rightarrow ProtD-NEF-TAT-HIS

DNA sequence

Nucleotides corresponding to the Prot D Fusion Partner are in bold.
 40

ATGGATCCAAGCAGCCATTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAA
 ATCATTATTGCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATAACGTTAGAATCT
 AAAGCACTTGCGTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACT
 AAGGATGGTCGTTTAGTGTTATTCACGATCACTTTTATAGATGGCTTGACTGATGTT
 45 GCGAAAAAATTCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTT

CLAIMS

1. An HIV NEF protein or derivative linked to an immunological fusion partner or
5 an HIV TAT protein.
2. HIV NEF-TAT fusion protein.
3. A protein as claimed in Claim 1 wherein the immunological fusion partner is a
10 Haemophilus Influenza B protein D or derivative thereof.
4. A Protein as claimed in Claim 1 wherein the fusion partner is a lipoprotein D or
derivative thereof.
- 15 5. A protein as claimed in Claim 3 or 4 wherein the fusion partner comprises
between 90-130 amino acid from the N terminal of protein D.
6. A protein as claimed in Claim 1 to 5, wherein the NEF protein is the entire
NEF protein.
20
7. A protein as claimed in Claim 1 to 6, wherein the NEF protein is fused to an
HIV TAT protein and an immunological fusion partner.
8. A protein as claimed in Claim 1 to 7, wherein the protein has a Histidine tail.
25
9. A nucleic acid encoding a protein of Claim 1 to 8.
10. A host transformed with a nucleic acid of Claim 9.
- 30 11. A vaccine comprising a protein of any of Claim 1 to 8 in admixture with a
pharmaceutically acceptable excipient.

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